

SEQUENCE LISTING



<110> Genencor International, Inc.
Bower, Benjamin
Mitchinson, Colin
Larenas, Edmund

<120> Cellulase Fusion Protein and Heterologous Cellulase Fusion
Construct Encoding the Same

<130> GC832-PCT

<140> PCT/US2005/010242

<141> 2005-03-25

<150> US 60/556,711

<151> 2004-03-25

<160> 30

<170> PatentIn version 3.2

<210> 1

<211> 1570

<212> DNA

<213> Trichoderma reesei

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<213> Trichoderma reesei

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Leu	Tyr	Phe	Val	Ser	Met	Asp	Ala	Asp	Gly	Gly	Val	Ser	Lys	Tyr	Pro
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Ala	Leu	Thr	Pro	His	Pro	Cys	Thr	Thr	Val	Gly	Gln	Glu	Ile	Cys	Glu
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 Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
 50 55 60
 Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
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 Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val
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 Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
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 Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
 115 120 125
 Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
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 Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
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 Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
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 Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
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 Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
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 Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
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 Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
 260 265 270
 Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
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 305 310 315 320
 Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala
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 Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe
 340 345 350
 Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp
 355 360 365
 Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn
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 Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser
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 <212> DNA
 <213> Acidothermus cellulolyticus

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 35 40 45
 Met Leu Asp Gln Ile Lys Ser Leu Gly Tyr Asn Thr Ile Arg Leu Pro
 50 55 60
 Tyr Ser Asp Asp Ile Leu Lys Pro Gly Thr Met Pro Asn Ser Ile Asn
 65 70 75 80
 Phe Tyr Gln Met Asn Gln Asp Leu Gln Gly Leu Thr Ser Leu Gln Val
 85 90 95
 Met Asp Lys Ile Val Ala Tyr Ala Gly Gln Ile Gly Leu Arg Ile Ile
 100 105 110
 Leu Asp Arg His Arg Pro Asp Cys Ser Gly Gln Ser Ala Leu Trp Tyr
 115 120 125
 Thr Ser Ser Val Ser Glu Ala Thr Trp Ile Ser Asp Leu Gln Ala Leu
 130 135 140
 Ala Gln Arg Tyr Lys Gly Asn Pro Thr Val Val Gly Phe Asp Leu His
 145 150 155 160
 Asn Glu Pro His Asp Pro Ala Cys Trp Gly Cys Gly Asp Pro Ser Ile

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Val Glu Thr Leu Ile Val Glu Ala Pro Asp Tyr Gly His Glu Thr Thr	
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130 135 140	
Met His Trp Leu Ala Asp Val Asp Asn Ile Tyr Gly Tyr Gly Asp Ser	
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Pro Gly Gly Gly Cys Glu Leu Gly Pro Ser Ala Lys Gly Val Ser Tyr	
165 170 175	
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Thr Gln Pro Thr Cys Asp Asn Gly Lys Tyr Gly Gly Ala His Gly Tyr	
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gccgtgccat	cgacgatctt	cacgtcacccg	gtgttcacga	ccggcaccag	cgctcgactat	1440
gcggaattga	atccgtcgat	catcgttcgc	gctggaagtt	tcgatccatc	gagccaaccg	1500
aacgacaggc	acgtcgcggt	ctcgacagac	ggcggcaaga	actggttcca	aggcagcgaa	1560
cctggcgggg	tgacgacggg	cggcaccgtc	gccgcacg	ccgacggctc	tcgtttcgtc	1620
tgggctccc	gcgatccccg	tcagcctgtg	gtgtacgcag	tcggatttgg	caactcctgg	1680
gctgcttcgc	aaggtgttcc	cgccaatgcc	cagatccgct	cagaccgggt	gaatccaaag	1740
actttctatg	ccctatccaa	tggaaccttc	tatcgaagca	cggacggcgg	cgtagacattc	1800
caaccggctg	cggccgggtc	tccgagcagc	ggtgccgtcg	gtgtcatgtt	ccacgcgggtg	1860
cctggaaaag	aaggcgatct	gtggctcgct	gcacgcagcg	ggctttacca	ctcaaccaat	1920
ggcggcagca	gttggtctgc	aatcaccggc	gtatcctccg	cggatgaacgt	gggatttggg	1980
aagtctgcgc	ccgggtcgtc	ataccagccg	gtctttgtcg	tcggcacgat	cggaggcggt	2040
acgggggctg	accgctccga	cgacgggtggg	acgacctggg	tacggatcaa	tgatgaccag	2100
caccaatacg	gaaattgggg	acaagcaatc	accggtgacc	cgcaatttta	cgggcgggtg	2160
tacataggca	cgaacggccg	tggaattgtc	tacggggaca	ttggtggtgc	gccgtccgga	2220
tcg						2223

<210> 12

<211> 741

<212> PRT

<213> Acidothermus cellulolyticus

<400> 12

Ala	Thr	Thr	Gln	Pro	Tyr	Thr	Trp	Ser	Asn	Val	Ala	Ile	Gly	Gly	Gly
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Gly	Phe	Val	Asp	Gly	Ile	Val	Phe	Asn	Glu	Gly	Ala	Pro	Gly	Ile	Leu
			20					25					30		
Tyr	Val	Arg	Thr	Asp	Ile	Gly	Gly	Met	Tyr	Arg	Trp	Asp	Ala	Ala	Asn
		35				40					45				
Gly	Arg	Trp	Ile	Pro	Leu	Leu	Asp	Trp	Val	Gly	Trp	Asn	Asn	Trp	Gly
	50					55					60				
Tyr	Asn	Gly	Val	Val	Ser	Ile	Ala	Ala	Asp	Pro	Ile	Asn	Thr	Asn	Lys
65					70				75					80	
Val	Trp	Ala	Ala	Val	Gly	Met	Tyr	Thr	Asn	Ser	Trp	Asp	Pro	Asn	Asp
			85						90					95	
Gly	Ala	Ile	Leu	Arg	Ser	Ser	Asp	Gln	Gly	Ala	Thr	Trp	Gln	Ile	Thr
			100					105					110		
Pro	Leu	Pro	Phe	Lys	Leu	Gly	Gly	Asn	Met	Pro	Gly	Arg	Gly	Met	Gly
		115					120				125				
Glu	Arg	Leu	Ala	Val	Asp	Pro	Asn	Asn	Asp	Asn	Ile	Leu	Tyr	Phe	Gly
	130					135					140				
Ala	Pro	Ser	Gly	Lys	Gly	Leu	Trp	Arg	Ser	Thr	Asp	Ser	Gly	Ala	Thr
145					150				155					160	
Trp	Ser	Gln	Met	Thr	Asn	Phe	Pro	Asp	Val	Gly	Thr	Tyr	Ile	Ala	Asn
			165					170					175		
Pro	Thr	Asp	Thr	Thr	Gly	Tyr	Gln	Ser	Asp	Ile	Gln	Gly	Val	Val	Trp
			180				185					190			
Val	Ala	Phe	Asp	Lys	Ser	Ser	Ser	Ser	Leu	Gly	Gln	Ala	Ser	Lys	Thr

		195					200					205				
Ile	Phe	Val	Gly	Val	Ala	Asp	Pro	Asn	Asn	Pro	Val	Phe	Trp	Ser	Arg	
	210					215					220					
Asp	Gly	Gly	Ala	Thr	Trp	Gln	Ala	Val	Pro	Gly	Ala	Pro	Thr	Gly	Phe	
225					230					235					240	
Ile	Pro	His	Lys	Gly	Val	Phe	Asp	Pro	Val	Asn	His	Val	Leu	Tyr	Ile	
				245					250					255		
Ala	Thr	Ser	Asn	Thr	Gly	Gly	Pro	Tyr	Asp	Gly	Ser	Ser	Gly	Asp	Val	
			260				265						270			
Trp	Lys	Phe	Ser	Val	Thr	Ser	Gly	Thr	Trp	Thr	Arg	Ile	Ser	Pro	Val	
		275					280					285				
Pro	Ser	Thr	Asp	Thr	Ala	Asn	Asp	Tyr	Phe	Gly	Tyr	Ser	Gly	Leu	Thr	
	290					295					300					
Ile	Asp	Arg	Gln	His	Pro	Asn	Thr	Ile	Met	Val	Ala	Thr	Gln	Ile	Ser	
305					310					315					320	
Trp	Trp	Pro	Asp	Thr	Ile	Ile	Phe	Arg	Ser	Thr	Asp	Gly	Gly	Ala	Thr	
				325					330					335		
Trp	Thr	Arg	Ile	Trp	Asp	Trp	Thr	Ser	Tyr	Pro	Asn	Arg	Ser	Leu	Arg	
			340				345						350			
Tyr	Val	Leu	Asp	Ile	Ser	Ala	Glu	Pro	Trp	Leu	Thr	Phe	Gly	Val	Gln	
		355					360					365				
Pro	Asn	Pro	Pro	Val	Pro	Ser	Pro	Lys	Leu	Gly	Trp	Met	Asp	Glu	Ala	
	370					375					380					
Met	Ala	Ile	Asp	Pro	Phe	Asn	Ser	Asp	Arg	Met	Leu	Tyr	Gly	Thr	Gly	
385					390					395					400	
Ala	Thr	Leu	Tyr	Ala	Thr	Asn	Asp	Leu	Thr	Lys	Trp	Asp	Ser	Gly	Gly	
				405					410					415		
Gln	Ile	His	Ile	Ala	Pro	Met	Val	Lys	Gly	Leu	Glu	Glu	Thr	Ala	Val	
			420					425					430			
Asn	Asp	Leu	Ile	Ser	Pro	Pro	Ser	Gly	Ala	Pro	Leu	Ile	Ser	Ala	Leu	
		435					440					445				
Gly	Asp	Leu	Gly	Gly	Phe	Thr	His	Ala	Asp	Val	Thr	Ala	Val	Pro	Ser	
	450					455					460					
Thr	Ile	Phe	Thr	Ser	Pro	Val	Phe	Thr	Thr	Gly	Thr	Ser	Val	Asp	Tyr	
465					470					475				480		
Ala	Glu	Leu	Asn	Pro	Ser	Ile	Ile	Val	Arg	Ala	Gly	Ser	Phe	Asp	Pro	
				485					490					495		
Ser	Ser	Gln	Pro	Asn	Asp	Arg	His	Val	Ala	Phe	Ser	Thr	Asp	Gly	Gly	
			500					505					510			
Lys	Asn	Trp	Phe	Gln	Gly	Ser	Glu	Pro	Gly	Gly	Val	Thr	Thr	Gly	Gly	
	515						520					525				
Thr	Val	Ala	Ala	Ser	Ala	Asp	Gly	Ser	Arg	Phe	Val	Trp	Ala	Pro	Gly	
	530					535					540					
Asp	Pro	Gly	Gln	Pro	Val	Val	Tyr	Ala	Val	Gly	Phe	Gly	Asn	Ser	Trp	
545					550					555						

Val Gly Phe Gly Lys Ser Ala Pro Gly Ser Ser Tyr Pro Ala Val Phe
 660 665 670
 Val Val Gly Thr Ile Gly Gly Val Thr Gly Ala Tyr Arg Ser Asp Asp
 675 680 685
 Gly Gly Thr Thr Trp Val Arg Ile Asn Asp Asp Gln His Gln Tyr Gly
 690 695 700
 Asn Trp Gly Gln Ala Ile Thr Gly Asp Pro Arg Ile Tyr Gly Arg Val
 705 710 715 720
 Tyr Ile Gly Thr Asn Gly Arg Gly Ile Val Tyr Gly Asp Ile Gly Gly
 725 730 735
 Ala Pro Ser Gly Ser
 740

<210> 13
 <211> 1677
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> construct based on *Thermobifida fusca*

<400> 13
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 accatcacca acctcggcag tgcgatcaac ggctggaccc tggagtggga cttccccggc 120
 aaccagcagg tgaccaacct gtggaacggg acctacaccc agtccgggca gcacgtgtcg 180
 gtcagcaacg ccccgtaaca cgcctccatc ccggccaacg gaacggttga gttcgggttc 240
 aacggctcct actcgggcag caacgacatc ccctcctcct tcaagctgaa cggggttacc 300
 tgcgacggct cggacgaccc cgaccccgag cccagccccct cccccagccc tccccccagc 360
 cccacagacc cggatgagcc gggcggcccg accaaccgcg ccaccaaccc cggcgagaag 420
 gtcgacaacc cgttcgaggg cgccaagctg tacgtgaacc cggctctggtc ggccaaggcc 480
 gccgctgagc cgggcggttc cgcggtcgcc aacgagtcca ccgctgtctg gctggaccgt 540
 atcggcgcca tcgagggcaa cgacagcccg accaccggct ccatgggtct gcgcgaccac 600
 ctggaggagg ccgtccgcca gtccggtggc gacccgctga ccatccaggt cgtcatctac 660
 aacctgcccg gccgcgactg cgccgcgctg gcctccaacg gtgagctggg tcccgatgaa 720
 ctcgaccgct acaagagcga gtacatcgac ccgatcgccg acatcatgtg ggacttcgca 780
 gactacgaga acctgcggat cgtcgccatc atcgagatcg actccctgcc caacctcgtc 840
 accaacgtgg gcgggaacgg cggcaccgag ctctgcgcct acatgaagca gaacggcggc 900
 tacgtcaacg gtgtcggcta cgccctccgc aagctgggcg agatcccga cgtctacaac 960
 tacatcgacg ccgcccacca cggctggatc ggctgggact ccaacttcgg cccctcggtg 1020
 gacatcttct acgagggcgc caacgcctcc ggctccaccg tggactacgt gcacggcttc 1080
 atctccaaca cggccaacta ctcggccact gtggagccgt acctggacgt caacggcacc 1140
 gttaacggcc agctcatccg ccagtccaag tgggttgact ggaaccagta cgtcgacgag 1200
 ctctccttcg tccaggacct gcgtcaggcc ctgatcgcca agggcttcg gtccgacatc 1260
 ggtatgctca tcgacacctc ccgcaacggc tgggggtggc cgaaccgtcc gaccggaccg 1320
 agtcctcca ccgacctcaa cactacgtt gacgagagcc gtatcgaccg ccgtatccac 1380
 cccggttaact ggtgcaacca ggccggtgcg ggccctcgcg agcggcccac ggtcaaccg 1440
 gctcccggtg ttgacgccta cgtctgggtg aagcccccg gtgagtcga cggcgccagc 1500
 gaggagatcc cgaacgacga gggcaaggcg ttcgaccgca tgtgcgaccc gacctaccg 1560
 ggcaacgccc gcaacggcaa caaccctcg ggtgcgtgc ccaacgcccc catctccggc 1620
 cactggttct ctgcccagtt ccgcgagctg ctggccaacg cctaccgcgc tctgtaa 1677

<210> 14
 <211> 558
 <212> PRT
 <213> Artificial Sequence

<220>

<223> construct based on Thermobifida fusca

<400> 14

Ala	Gly	Cys	Ser	Val	Asp	Tyr	Thr	Val	Asn	Ser	Trp	Gly	Thr	Gly	Phe
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Thr	Ala	Asn	Val	Thr	Ile	Thr	Asn	Leu	Gly	Ser	Ala	Ile	Asn	Gly	Trp
			20					25					30		
Thr	Leu	Glu	Trp	Asp	Phe	Pro	Gly	Asn	Gln	Gln	Val	Thr	Asn	Leu	Trp
		35					40					45			
Asn	Gly	Thr	Tyr	Thr	Gln	Ser	Gly	Gln	His	Val	Ser	Val	Ser	Asn	Ala
	50					55					60				
Pro	Tyr	Asn	Ala	Ser	Ile	Pro	Ala	Asn	Gly	Thr	Val	Glu	Phe	Gly	Phe
65					70					75					80
Asn	Gly	Ser	Tyr	Ser	Gly	Ser	Asn	Asp	Ile	Pro	Ser	Ser	Phe	Lys	Leu
				85					90					95	
Asn	Gly	Val	Thr	Cys	Asp	Gly	Ser	Asp	Asp	Pro	Asp	Pro	Glu	Pro	Ser
			100					105					110		
Pro	Ser	Pro	Ser	Pro	Ser	Pro	Ser	Pro	Thr	Asp	Pro	Asp	Glu	Pro	Gly
		115					120					125			
Gly	Pro	Thr	Asn	Pro	Pro	Thr	Asn	Pro	Gly	Glu	Lys	Val	Asp	Asn	Pro
	130					135						140			
Phe	Glu	Gly	Ala	Lys	Leu	Tyr	Val	Asn	Pro	Val	Trp	Ser	Ala	Lys	Ala
145					150					155					160
Ala	Ala	Glu	Pro	Gly	Gly	Ser	Ala	Val	Ala	Asn	Glu	Ser	Thr	Ala	Val
				165					170					175	
Trp	Leu	Asp	Arg	Ile	Gly	Ala	Ile	Glu	Gly	Asn	Asp	Ser	Pro	Thr	Thr
		180						185					190		
Gly	Ser	Met	Gly	Leu	Arg	Asp	His	Leu	Glu	Glu	Ala	Val	Arg	Gln	Ser
		195					200					205			
Gly	Gly	Asp	Pro	Leu	Thr	Ile	Gln	Val	Val	Ile	Tyr	Asn	Leu	Pro	Gly
	210					215					220				
Arg	Asp	Cys	Ala	Ala	Leu	Ala	Ser	Asn	Gly	Glu	Leu	Gly	Pro	Asp	Glu
225					230					235					240
Leu	Asp	Arg	Tyr	Lys	Ser	Glu	Tyr	Ile	Asp	Pro	Ile	Ala	Asp	Ile	Met
				245					250					255	
Trp	Asp	Phe	Ala	Asp	Tyr	Glu	Asn	Leu	Arg	Ile	Val	Ala	Ile	Ile	Glu
		260						265					270		
Ile	Asp	Ser	Leu	Pro	Asn	Leu	Val	Thr	Asn	Val	Gly	Gly	Asn	Gly	Gly
		275					280					285			
Thr	Glu	Leu	Cys	Ala	Tyr	Met	Lys	Gln	Asn	Gly	Gly	Tyr	Val	Asn	Gly
	290					295					300				
Val	Gly	Tyr	Ala	Leu	Arg	Lys	Leu	Gly	Glu	Ile	Pro	Asn	Val	Tyr	Asn
305					310					315					320
Tyr	Ile	Asp	Ala	Ala	His	His	Gly	Trp	Ile	Gly	Trp	Asp	Ser	Asn	Phe
				325					330					335	
Gly	Pro	Ser	Val	Asp	Ile	Phe	Tyr	Glu	Ala	Ala	Asn	Ala	Ser	Gly	Ser
			340					345					350		
Thr	Val	Asp	Tyr	Val	His	Gly	Phe	Ile	Ser	Asn	Thr	Ala	Asn	Tyr	Ser
		355					360					365			
Ala	Thr	Val	Glu	Pro	Tyr	Leu	Asp	Val	Asn	Gly	Thr	Val	Asn	Gly	Gln
	370					375					380				
Leu	Ile	Arg	Gln	Ser	Lys	Trp	Val	Asp	Trp	Asn	Gln	Tyr	Val	Asp	Glu
385					390					395					400
Leu	Ser	Phe	Val	Gln	Asp	Leu	Arg	Gln	Ala	Leu	Ile	Ala	Lys	Gly	Phe
				405					410					415	
Arg	Ser	Asp	Ile	Gly	Met	Leu	Ile	Asp	Thr	Ser	Arg	Asn	Gly	Trp	Gly
			420					425					430		

Gly	Pro	Asn	Arg	Pro	Thr	Gly	Pro	Ser	Ser	Ser	Thr	Asp	Leu	Asn	Thr
		435					440					445			
Tyr	Val	Asp	Glu	Ser	Arg	Ile	Asp	Arg	Arg	Ile	His	Pro	Gly	Asn	Trp
	450					455					460				
Cys	Asn	Gln	Ala	Gly	Ala	Gly	Leu	Gly	Glu	Arg	Pro	Thr	Val	Asn	Pro
465					470					475					480
Ala	Pro	Gly	Val	Asp	Ala	Tyr	Val	Trp	Val	Lys	Pro	Pro	Gly	Glu	Ser
			485						490					495	
Asp	Gly	Ala	Ser	Glu	Glu	Ile	Pro	Asn	Asp	Glu	Gly	Lys	Gly	Phe	Asp
			500					505					510		
Arg	Met	Cys	Asp	Pro	Thr	Tyr	Gln	Gly	Asn	Ala	Arg	Asn	Gly	Asn	Asn
		515					520					525			
Pro	Ser	Gly	Ala	Leu	Pro	Asn	Ala	Pro	Ile	Ser	Gly	His	Trp	Phe	Ser
	530					535					540				
Ala	Gln	Phe	Arg	Glu	Leu	Leu	Ala	Asn	Ala	Tyr	Pro	Pro	Leu		
545					550					555					

<210> 15
 <211> 1293
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> construct based on *Thermobifida fusca*

<400> 15

gccggtcttc	ccgccacagt	caccaaagaa	tcctcgtggg	acaacggcta	ctccgcgtcc	60
gtcaccgtcc	gcaacgacac	ctcgagcacc	gtctcccagt	gggaggtcgt	cctcaccctg	120
cccggcgcca	ctacagtggc	ccaggtgtgg	aacgcccagc	acaccagcag	cggcaactcc	180
cacaccttca	ccggggtttc	ctggaacagc	accatcccgc	ccggaggcac	cgcctcttcc	240
ggcttcatcg	cttccggcag	cggcgaaccc	acccactgca	ccatcaacgg	cgccccctgc	300
gacgaaggct	ccgagccggg	cggccccggc	ggtcccggaa	ccccctcccc	cgaccccggc	360
acgcagcccc	gcaccggcac	cccggtcgag	cggtagcgca	aagtccaggt	ctgcggcacc	420
cagctctgcg	acgagcacgg	caaccgggtc	caactgcgcg	gcatgagcac	ccacggcatc	480
cagtggttcg	accactgcct	gaccgacagc	tcgctggacg	ccctggccta	cgactggaag	540
gccgacatca	tccgcctgtc	catgtacatc	caggaagacg	gctacgagac	caaccgcgcg	600
ggcttcaccg	accggatgca	ccagctcatc	gacatggcca	cggcgcgcgg	cctgtacgtg	660
atcgtaggact	ggcacatcct	caccccgggc	gatccccact	acaacctgga	ccggggccaag	720
accttcttcg	cggaaatcgc	ccagcgccac	gccagcaaga	ccaacgtgct	ctacgagatc	780
gccaacgaac	ccaacggagt	gagctggggc	tccatcaaga	gctacgccga	agaggtcatc	840
ccggtgatcc	gccagcgcca	ccccgactcg	gtgatcatcg	tgggcacccg	cggctggctg	900
tcgctcggcg	tctccgaagg	ctccggcccc	gccgagatcg	cggccaaccc	ggtcaacgcc	960
tccaacatca	tgtacgcctt	ccacttctac	gcggcctcgc	accgcgacaa	ctacctcaac	1020
gcgctgcgtg	aggcctccga	gctgttcccc	gtcttcgtca	ccgagttcgg	caccgagacc	1080
tacaccggtg	acggcgccaa	cgacttcag	atggccgacc	gctacatcga	cctgatggcg	1140
gaacggaaga	tcgggtggac	caagtggaac	tactcggacg	acttcggttc	cggcgcggtc	1200
ttccagccgg	gcacctgcgc	gtccggcggc	ccgtggagcg	gttcgtcgtc	gaaggcgtcc	1260
ggacagtggg	tgcygagcaa	gtccagtc	tga			1293

<210> 16
 <211> 430
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> construct based on *Thermobifida fusca*

<400> 16

Ala	Gly	Leu	Thr	Ala	Thr	Val	Thr	Lys	Glu	Ser	Ser	Trp	Asp	Asn	Gly	
1				5					10					15		
Tyr	Ser	Ala	Ser	Val	Thr	Val	Arg	Asn	Asp	Thr	Ser	Ser	Thr	Val	Ser	
			20					25					30			
Gln	Trp	Glu	Val	Val	Leu	Thr	Leu	Pro	Gly	Gly	Thr	Thr	Val	Ala	Gln	
		35					40					45				
Val	Trp	Asn	Ala	Gln	His	Thr	Ser	Ser	Gly	Asn	Ser	His	Thr	Phe	Thr	
	50					55					60					
Gly	Val	Ser	Trp	Asn	Ser	Thr	Ile	Pro	Pro	Gly	Gly	Thr	Ala	Ser	Ser	
65					70					75					80	
Gly	Phe	Ile	Ala	Ser	Gly	Ser	Gly	Glu	Pro	Thr	His	Cys	Thr	Ile	Asn	
				85					90					95		
Gly	Ala	Pro	Cys	Asp	Glu	Gly	Ser	Glu	Pro	Gly	Gly	Pro	Gly	Gly	Pro	
			100					105					110			
Gly	Thr	Pro	Ser	Pro	Asp	Pro	Gly	Thr	Gln	Pro	Gly	Thr	Gly	Thr	Pro	
		115					120					125				
Val	Glu	Arg	Tyr	Gly	Lys	Val	Gln	Val	Cys	Gly	Thr	Gln	Leu	Cys	Asp	
	130					135					140					
Glu	His	Gly	Asn	Pro	Val	Gln	Leu	Arg	Gly	Met	Ser	Thr	His	Gly	Ile	
145					150					155					160	
Gln	Trp	Phe	Asp	His	Cys	Leu	Thr	Asp	Ser	Ser	Leu	Asp	Ala	Leu	Ala	
				165					170					175		
Tyr	Asp	Trp	Lys	Ala	Asp	Ile	Ile	Arg	Leu	Ser	Met	Tyr	Ile	Gln	Glu	
			180					185					190			
Asp	Gly	Tyr	Glu	Thr	Asn	Pro	Arg	Gly	Phe	Thr	Asp	Arg	Met	His	Gln	
		195					200					205				
Leu	Ile	Asp	Met	Ala	Thr	Ala	Arg	Gly	Leu	Tyr	Val	Ile	Val	Asp	Trp	
	210					215					220					
His	Ile	Leu	Thr	Pro	Gly	Asp	Pro	His	Tyr	Asn	Leu	Asp	Arg	Ala	Lys	
225					230					235					240	
Thr	Phe	Phe	Ala	Glu	Ile	Ala	Gln	Arg	His	Ala	Ser	Lys	Thr	Asn	Val	
			245						250					255		
Leu	Tyr	Glu	Ile	Ala	Asn	Glu	Pro	Asn	Gly	Val	Ser	Trp	Ala	Ser	Ile	
		260						265					270			
Lys	Ser	Tyr	Ala	Glu	Glu	Val	Ile	Pro	Val	Ile	Arg	Gln	Arg	Asp	Pro	
		275					280					285				
Asp	Ser	Val	Ile	Ile	Val	Gly	Thr	Arg	Gly	Trp	Ser	Ser	Leu	Gly	Val	
	290					295					300					
Ser	Glu	Gly	Ser	Gly	Pro	Ala	Glu	Ile	Ala	Ala	Asn	Pro	Val	Asn	Ala	
305					310					315					320	
Ser	Asn	Ile	Met	Tyr	Ala	Phe	His	Phe	Tyr	Ala	Ala	Ser	His	Arg	Asp	
			325						330					335		
Asn	Tyr	Leu	Asn	Ala	Leu	Arg	Glu	Ala	Ser	Glu	Leu	Phe	Pro	Val	Phe	
		340						345					350			
Val	Thr	Glu	Phe	Gly	Thr	Glu	Thr	Tyr	Thr	Gly	Asp	Gly	Ala	Asn	Asp	
		355					360					365				
Phe	Gln	Met	Ala	Asp	Arg	Tyr	Ile	Asp	Leu	Met	Ala	Glu	Arg	Lys	Ile	
	370					375					380					
Gly	Trp	Thr	Lys	Trp	Asn	Tyr	Ser	Asp	Asp	Phe	Arg	Ser	Gly	Ala	Val	
385					390					395					400	
Phe	Gln	Pro	Gly	Thr	Cys	Ala	Ser	Gly	Gly	Pro	Trp	Ser	Gly	Ser	Ser	
			405						410					415		
Leu	Lys	Ala	Ser	Gly	Gln	Trp	Val	Arg	Ser	Lys	Leu	Gln	Ser			
		420						425					430			

<210> 17

<211> 2656
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion construct

<400> 17
 atgtatcggga agttggccgt catctcggcc ttcttggcca cagctcgtgc tcagtcggcc 60
 tgcactctcc aatcggagac tcacccgcct ctgacatggc agaaatgctc gtctgggtggc 120
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<210> 18
 <211> 841
 <212> PRT

<213> Artificial Sequence

<220>

<223> fusion construct

<400> 18

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 <213> Artificial Sequence

<220>
 <223> pTrex plasmid

<400> 19

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